

Fig. 1

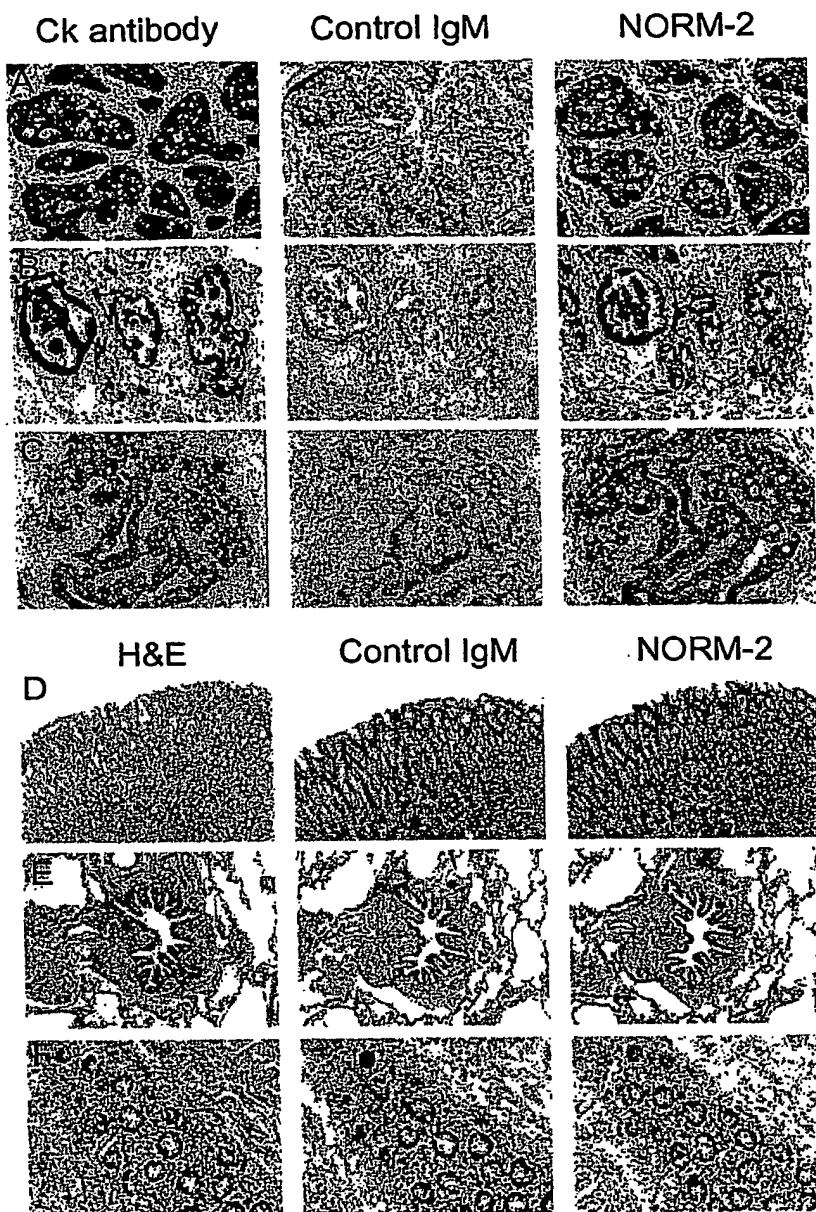


Fig. 2

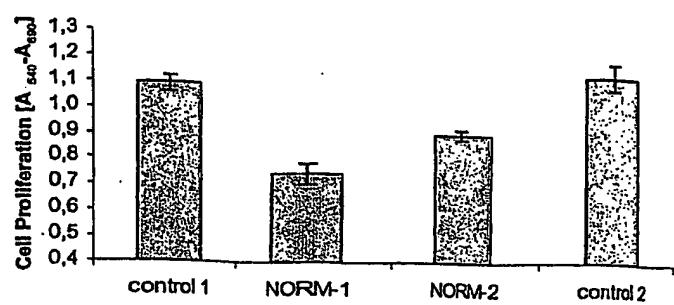


Fig. 3

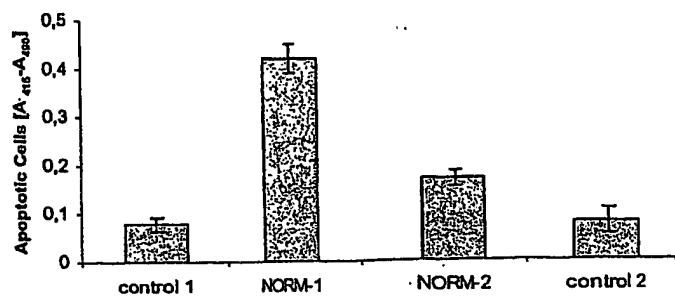


Fig. 4

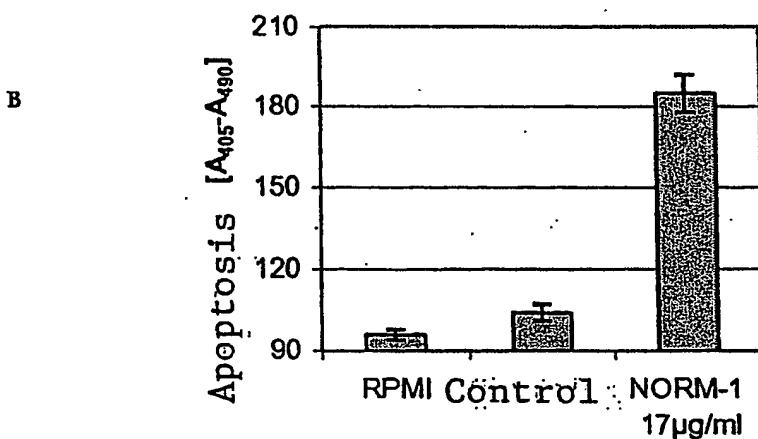
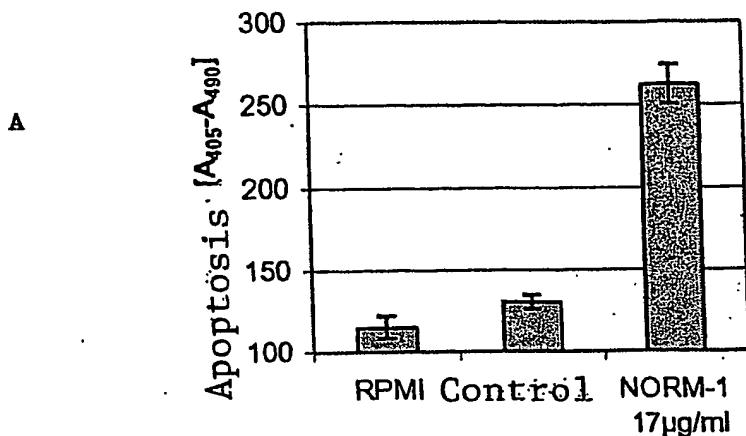


Fig. 5

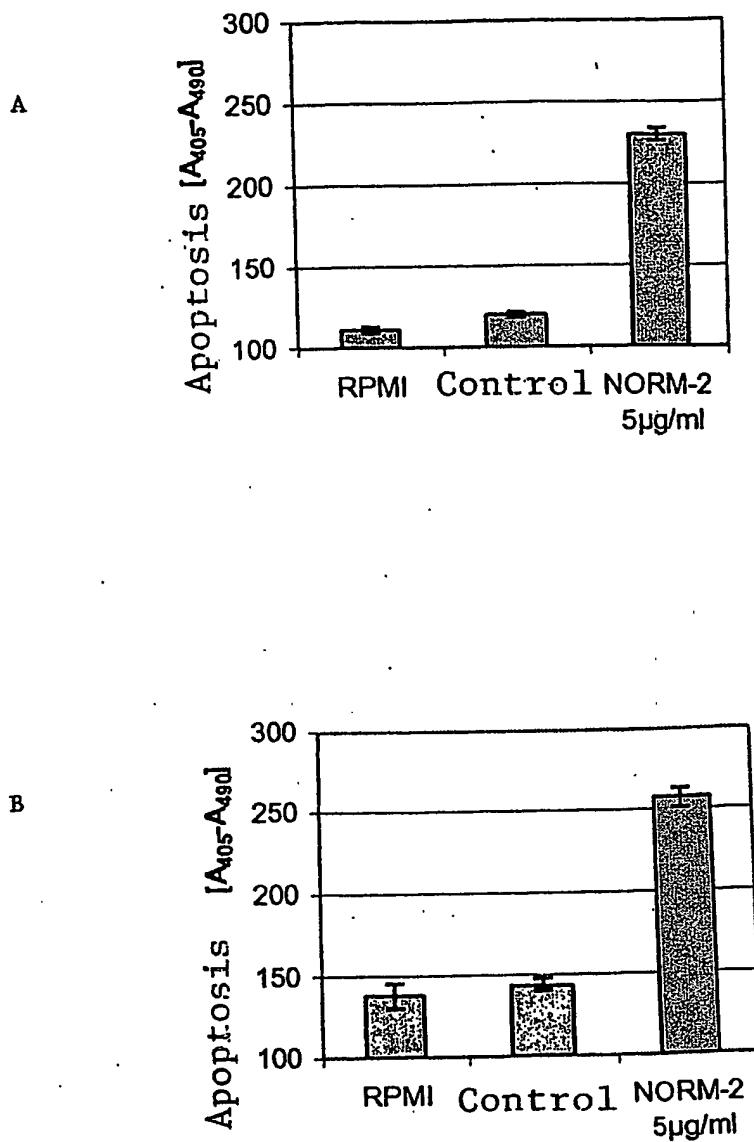


Fig. 6

NORM-1 (VH)

GAG	GTG	CAG	CTG	TRG	TRG	GAG	TCT	GGG	GGG	GGC	TTG	GTG	CAG	CCT	GGG	GGG	TCC	CTG	AGA	CTC	
Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu		
1		5		10				15		20										60	
CDR1																					
TCC	TGT	GCA	GCC	TCT	GGG	TTC	ACC	TTT	AGC	AGC	TAT	GCC	ATG	AGC	91	105	TGG	GTC	CGC	CAG	GCT
Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Ala	Met	Ser	30	35	Trp	Val	Arg	Gln	Ala
25		30																		40	
CDR2																					
CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCA	GCT	GCT	ATT	AGT	GGT	GGT	148	180	AGC	ACA	TAC	TAC	TAC
Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Ala	Ile	Ser	Gly	Ser	Gly	50	55	Thr	Tyr	Tyr	Tyr	Tyr
																	60				
CDR3																					
GCA	GAC	TCC	GTG	AAG	GGC	CGG	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	198	240	AAG	AAC	ACG	CTG	TAT
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	65	70	Lys	Asn	Thr	Leu	Tyr
																	80				
D-Region																					
CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	ACG	GCC	GTC	TAT	TAC	295	300	GCG	AAA	GAT	GGC	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	95	90	Cys	Ala	Lys	Asp	Gly
																	100				
J-Region																					
TAT	GAT	AGT	AGT	GGT	TAT	TCG	GAA	TAT	TAC	TAC	TAC	TAC	ATG	GAC	321	357	GGC				
Tyr	Asp	Ser	Ser	Gly	Tyr	Ser	Glu	Glu	Tyr	Tyr	Tyr	Tyr	Met	Asp	105	110	Val	(Seq. ID. No: 2)	(Seq. ID. No: 1)		
																				115	

NORM-1 (VL)

TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG TCC CCA GGA CAA ACG GCC AGG ATC
 Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gln Thr Ala Arg Ile
 1 5 10 15 20
 CDR1 67 99
 ACC TGC TCT GGA GAT GCA TGT CCA AAA AAA TAT GCT TAT TGG TAC CAG CAG AAG TCA GGG
 Thr Cys Ser Gly Asp Ala Leu Pro Lys Lys Tyr Ala Tyr Trp Tyr Gln Gln Lys Ser Gly
 25 30 35 40
 CDR2 145 165
 CAG GCC CCT GTG CTG GTC ATC TAT GAG GAC AGC AAA CGA CCC TCC GGG ATC CCT GAG AGA
 Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
 45 50 55 60
 CDR3 262 297
 TTC TCT GGC TCC AGC TCA GGG ACA ATG GCC ACC TTG ACT ATC AGT GGG GCC CAG GTG GAG
 Phe Ser Gly Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
 65 70 75 80
 J-Region
 GAT GAA GCT GAC TAC TAC TGT TAC TCA ACA GAC AGC AGT GGT AAT CAT AGC TAT GTG TTC (SEQ. ID. NO: 4) 300
 Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Gln Asn His Ser Tyr Val Phe (SEQ. ID. NO: 3)
 85 90 95 100

NORM-2 (VH)

NORM-2 (VL)

CAG TCT GTC TCG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG AGG GTC ACC ATC 60
 Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile 20
 1 5 10 15 20
 TCC TGC ACT GGG AGC TCC AAC ATC GGG GCA GGT TAT GAT GTA CAC TGG TAC CAG CAG 108
 Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln 40
 25 30 35 40
 CDR1

CCT CCA GGA ACA GCC CCC AAA CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC 174
 Leu Pro Gly Thr Ala Pro Lys Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val 60
 45 50 55 60
 CDR2

CCT GAC CGG TTC TCT GGC TCC AAG TCT GGC ACC TCA GGC TCC TCG GCC ACT GGG CTC 240
 Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Ile Thr Gly Leu 80
 65 70 75 80
 J-Region

CAG GCT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT GCC TTG 300
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Ala Leu 95
 85 90 95
 CDR3

GTC TTC (seq. ID. no: 8)
 Val Phe (seq. ID. no: 7)

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